



SEQUENCE LISTING

<110> Yeatman, Timothy J.
Irby, Rosalyn B.

<120> Mutated SRC Oncogene Composition and Methods

<130> USF-T136

<140> US 09/444,711

<141> 1999-11-24

<160> 7

<170> PatentIn version 3.1

<210> 1

<211> 1611

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(1611)

<223> nucleotide sequence of normal c-Src oncogene coding region

<220>

<221> CDS

<222> (1)..(1611)

<223>

<400> 1

atg ggt agc aac aag agc aag ccc aag gat gcc agc cag cgg cgc cgc 48
Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg
1 5 10 15

agc ctg gag ccc gcc gag aac gtg cac ggc gct ggc ggg ggc gct ttc 96
Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe
20 25 30

ccc gcc tcg cag acc ccc agc aag cca gcc tcg gcc gac ggc cac cgc 144
Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg
35 40 45

ggc ccc agc gcg gcc ttc gcc ccc gcg gcc gcc gag ccc aag ctg ttc 192
Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe
50 55 60

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gga ggc ttc aac tcc tcg gac acc gtc acc tcc ccg cag agg gcg ggc 240
 Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly
 65 70 75 80

ccg ctg gcc ggt gga gtg acc acc ttt gtg gcc ctc tat gac tat gag 288
 Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu
 85 90 95

tct agg acg gag aca gac ctg tcc ttc aag aaa ggc gag cgg ctc cag 336
 Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln
 100 105 110

att gtc aac aac acg gag gga gac tgg tgg ctg gcc cac tcg ctc agc 384
 Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser
 115 120 125

aca gga cag aca ggc tac atc ccc agc aac tac gtg gcg ccc tcc gac 432
 Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp
 130 135 140

tcc atc cag gct gag gag tgg tat ttt ggc aag atc acc aga cgg gag 480
 Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu
 145 150 155 160

tca gag cgg tta ctg ctc aat gca gag aac ccg aga ggg acc ttc ctc 528
 Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu
 165 170 175

gtg cga gaa agt gag acc acg aaa ggt gcc tac tgc ctc tca gtg tct 576
 Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser
 180 185 190

gac ttc gac aac gcc aag ggc ctc aac gtg aag cac tac aag atc cgc 624
 Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg
 195 200 205

aag ctg gac agc ggc ggc ttc tac atc acc tcc cgc acc cag ttc aac 672
 Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn
 210 215 220

agc ctg cag cag ctg gtg gcc tac tac tcc aaa cac gcc gat ggc ctg 720
 Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu
 225 230 235 240

tgc cac cgc ctc acc acc gtg tgc ccc acg tcc aag ccg cag act cag 768
 Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln
 245 250 255

ggc ctg gcc aag gat gcc tgg gag atc cct cgg gag tcg ctg cgg ctg 816
 Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu
 260 265 270

gag gtc aag ctg ggc cag ggc tgc ttt ggc gag gtg tgg atg ggg acc	864
Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr	
275 280 285	
tgg aac ggt acc acc agg gtg gcc atc aaa acc ctg aag cct ggc acg	912
Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr	
290 295 300	
atg tct cca gag gcc ttc ctg cag gag gcc cag gtc atg aag aag ctg	960
Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu	
305 310 315 320	
agg cat gag aag ctg gtg cag ttg tat gct gtg gtt tca gag gag ccc	1008
Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro	
325 330 335	
att tac atc gtc acg gag tac atg agc aag ggg agt ttg ctg gac ttt	1056
Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe	
340 345 350	
ctc aag ggg gag aca ggc aag tac ctg cgg ctg cct cag ctg gtg gac	1104
Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp	
355 360 365	
atg gct gct cag atc gcc tca ggc atg gcg tac gtg gag cgg atg aac	1152
Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn	
370 375 380	
tac gtc cac cgg gac ctt cgt gca gcc aac atc ctg gtg gga gag aac	1200
Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn	
385 390 395 400	
ctg gtg tgc aaa gtg gcc gac ttt ggg ctg gct cgg ctc att gaa gac	1248
Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp	
405 410 415	
aat gag tac acg gcg cgg caa ggt gcc aaa ttc ccc atc aag tgg acg	1296
Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr	
420 425 430	
gct cca gaa gct gcc ctc tat ggc cgc ttc acc atc aag tcg gac gtg	1344
Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val	
435 440 445	
tgg tcc ttc ggg atc ctg ctg act gag ctc acc aca aag gga cgg gtg	1392
Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val	
450 455 460	
ccc tac cct ggg atg gtg aac cgc gag gtg ctg gac cag gtg gag cgg	1440
Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg	
465 470 475 480	
ggc tac cgg atg ccc tgc ccg ccg gag tgt ccc gag tcc ctg cac gac	1488
Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp	
485 490 495	

ctc atg tgc cag tgc tgg cgg aag gag cct gag gag cgg ccc acc ttc 1536
 Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe
 500 505 510

gag tac ctg cag gcc ttc ctg gag gac tac ttc acg tcc acc gag ccc 1584
 Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro
 515 520 525

cag tac cag ccc ggg gag aac ctc tag 1611
 Gln Tyr Gln Pro Gly Glu Asn Leu
 530 535

<210> 2
 <211> 536
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(536)
 <223> amino acid sequence of non-receptor tyrosine kinase encoded
 by the normal c-Src coding region

<400> 2
 Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg
 1 5 10 15

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe
 20 25 30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg
 35 40 45

Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe
 50 55 60

Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly
 65 70 75 80

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu
 85 90 95

Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln
 100 105 110

Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser
 115 120 125

Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp
 130 135 140

Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu
 145 150 155 160

Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu
 165 170 175
 Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser
 180 185 190
 Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg
 195 200 205
 Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn
 210 215 220
 Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu
 225 230 235 240
 Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln
 245 250 255
 Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu
 260 265 270
 Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr
 275 280 285
 Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr
 290 295 300
 Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu
 305 310 315 320
 Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
 325 330 335
 Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe
 340 345 350
 Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp
 355 360 365
 Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn
 370 375 380
 Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn
 385 390 395 400
 Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
 405 410 415
 Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
 420 425 430
 Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val
 435 440 445
 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val
 450 455 460

Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg
465 470 475 480

Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp
485 490 495

Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe
500 505 510

Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro
515 520 525

Gln Tyr Gln Pro Gly Glu Asn Leu
530 535

<210> 3
<211> 1611
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(1593)
<223> nucleotide sequence of mutant c-Src oncogene coding region

<220>
<221> CDS
<222> (1)..(1593)
<223>

<220>
<221> misc_feature
<222> (1591)..(1591)
<223> Point mutation in normal c-Src causes transition from c-->t and the formation of a stop codon.

<400> 3
atg ggt agc aac aag agc aag ccc aag gat gcc agc cag cgg cgc cgc 48
Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg
1 5 10 15

agc ctg gag ccc gcc gag aac gtg cac ggc gct ggc ggg ggc gct ttc 96
Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe
20 25 30

ccc gcc tcg cag acc ccc agc aag cca gcc tcg gcc gac ggc cac cgc 144
Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg
35 40 45

ggc ccc agc gcg gcc ttc gcc ccc gcg gcc gcc gag ccc aag ctg ttc 192
Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe
50 55 60

gga ggc ttc aac tcc tcg gac acc gtc acc tcc ccg cag agg gcg ggc 240
 Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly
 65 70 75 80

ccg ctg gcc ggt gga gtg acc acc ttt gtg gcc ctc tat gac tat gag 288
 Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu
 85 90 95

tct agg acg gag aca gac ctg tcc ttc aag aaa ggc gag cgg ctc cag 336
 Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln
 100 105 110

att gtc aac aac acg gag gga gac tgg tgg ctg gcc cac tcg ctc agc 384
 Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser
 115 120 125

aca gga cag aca ggc tac atc ccc agc aac tac gtg gcg ccc tcc gac 432
 Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp
 130 135 140

tcc atc cag gct gag gag tgg tat ttt ggc aag atc acc aga cgg gag 480
 Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu
 145 150 155 160

tca gag cgg tta ctg ctc aat gca gag aac ccg aga ggg acc ttc ctc 528
 Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu
 165 170 175

gtg cga gaa agt gag acc acg aaa ggt gcc tac tgc ctc tca gtg tct 576
 Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser
 180 185 190

gag ttc gag aac gcc aag ggc ctc aac gtg aag cac tac aag atc cgc 624
 Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg
 195 200 205

aag ctg gac agc ggc ggc ttc tac atc acc tcc cgc acc cag ttc aac 672
 Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn
 210 215 220

agc ctg cag cag ctg gtg gcc tac tac tcc aaa cac gcc gat ggc ctg 720
 Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu
 225 230 235 240

tgc cac cgc ctc acc acc gtg tgc ccc acg tcc aag ccg cag act cag 768
 Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln
 245 250 255

ggc ctg gcc aag gat gcc tgg gag atc cct cgg gag tcg ctg cgg ctg 816
 Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu
 260 265 270

gag gtc aag ctg ggc cag ggc tgc ttt ggc gag gtg tgg atg ggg acc 864
 Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr
 275 280 285

tgg aac ggt acc acc agg gtg gcc atc aaa acc ctg aag cct ggc acg 912
 Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr
 290 295 300

atg tct cca gag gcc ttc ctg cag gag gcc cag gtc atg aag aag ctg 960
 Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu
 305 310 315 320

agg cat gag aag ctg gtg cag ttg tat gct gtg gtt tca gag gag ccc 1008
 Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
 325 330 335

att tac atc gtc acg gag tac atg agc aag ggg agt ttg ctg gac ttt 1056
 Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe
 340 345 350

ctc aag ggg gag aca ggc aag tac ctg cgg ctg cct cag ctg gtg gac 1104
 Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp
 355 360 365

atg gct gct cag atc gcc tca ggc atg gcg tac gtg gag cgg atg aac 1152
 Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn
 370 375 380

tac gtc cac cgg gac ctt cgt gca gcc aac atc ctg gtg gga gag aac 1200
 Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn
 385 390 395 400

ctg gtg tgc aaa gtg gcc gac ttt ggg ctg gct cgg ctc att gaa gac 1248
 Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
 405 410 415

aat gag tac acg gcg cgg caa ggt gcc aaa ttc ccc atc aag tgg acg 1296
 Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
 420 425 430

gct cca gaa gct gcc ctc tat ggc cgc ttc acc atc aag tcg gac gtg 1344
 Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val
 435 440 445

tgg tcc ttc ggg atc ctg ctg act gag ctc acc aca aag gga cgg gtg 1392
 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val
 450 455 460

ccc tac cct ggg atg gtg aac cgc gag gtg ctg gac cag gtg gag cgg 1440
 Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg
 465 470 475 480

ggc tac cgg atg ccc tgc ccg ccg gag tgt ccc gag tcc ctg cac gac 1488
 Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp
 485 490 495

ctc atg tgc cag tgc tgg cgg aag gag cct gag gag cgg ccc acc ttc 1536
 Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe
 500 505 510

gag tac ctg cag gcc ttc ctg gag gac tac ttc acg tcc acc gag ccc 1584
 Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro
 515 520 525

cag tac tag cccggggaga acctctag 1611
 Gln Tyr
 530

<210> 4
 <211> 530
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(530)
 <223> amino acid sequence of the mutant c-Src polypeptide encoded
 by the mutant c-Src coding region

<400> 4
 Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg
 1 5 10 15

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe
 20 25 30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg
 35 40 45

Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe
 50 55 60

Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly
 65 70 75 80

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu
 85 90 95

Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln
 100 105 110

Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser
 115 120 125

Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp
 130 135 140

Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu
 145 150 155 160

Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu
 165 170 175

Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser
 180 185 190
 Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg
 195 200 205
 Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn
 210 215 220
 Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu
 225 230 235 240
 Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln
 245 250 255
 Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu
 260 265 270
 Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr
 275 280 285
 Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr
 290 295 300
 Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu
 305 310 315 320
 Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
 325 330 335
 Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe
 340 345 350
 Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp
 355 360 365
 Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn
 370 375 380
 Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn
 385 390 395 400
 Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
 405 410 415
 Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
 420 425 430
 Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val
 435 440 445
 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val
 450 455 460
 Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg
 465 470 475 480

Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp
 485 490 495

Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe
 500 505 510

Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro
 515 520 525

Gln Tyr
 530

<210> 5
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 3' mutant allele specific primer
 <220>
 <221> misc_feature

<222> (15)..(15)
 <223> n is defined as a 3-nitropyrrole residue

<400> 5
 tagaggttct ccccnnggcta

20

<210> 6
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 3' wild-type allele specific primer

<400> 6
 tagaggttct ccccgggctg

20

<210> 7
 <211> 164
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Antisense sequence complementary to 5' region of c-Src gene

<400> 7

gccccgcagg tgctactgc ctctcagtgt ctgacttcga caacgccaaag ggcctcaacg 60

tgaagcacta caagatccgc aagctggaca gcggcggctt ctacatcacc tcccgcaccc 120

agttcaacag cctgcagcag ctggtggcct actactccag tgag 164

Ch